Amendments to the Specification:

Please replace the paragraph on page 31, lines 10-24, with the following amended paragraph:

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least a portion of, for example, approximately 6, 12, 15, 20, 30, 50, 100, 150, 200, 300, 350, 400, 500, 750, or 1000 contiguous nucleotides of a nucleic acid designated in ~~any one of SEQ ID Nos: 1-146~~ Table 1, or a sequence complementary thereto, or naturally occurring mutants thereof, such that it has less than 15%, preferably less than 10%, and more preferably less than 5% background hybridization to a cellular nucleic acid (e.g., mRNA or genomic DNA) encoding a different protein. In preferred embodiments, the oligonucleotide probe detects only a specific nucleic acid, e.g., it does not substantially hybridize to similar or related nucleic acids, or complements thereof.

Please replace the paragraph on page 85, lines 4-29, with the following amended paragraph:

In yet another embodiment, the invention provides methods for determining whether a subject is at risk for developing a disease, such as a predisposition to develop IBD, for example UC or CD, associated with an aberrant activity of any one of the polypeptides encoded by nucleic acids of ~~SEQ ID Nos: 1-146~~ Table 1, wherein the aberrant activity of the polypeptide is characterized by detecting the presence or absence of a genetic lesion characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a marker polypeptides, or (ii) the mis-expression of the encoding nucleic acid. To illustrate, such genetic lesions can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from the nucleic acid sequence, (ii) an addition of one or more nucleotides to the nucleic acid sequence, (iii) a substitution of one or more nucleotides of the nucleic acid sequence, (iv) a gross chromosomal rearrangement of the nucleic acid sequence, (v) a gross alteration in the level of a messenger RNA transcript of the nucleic acid sequence, (vii) aberrant modification of the nucleic acid sequence, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene, (viii) a non-wild type

level of the marker polypeptide, (ix) allelic loss of the gene, and/or (x) inappropriate post-translational modification of the marker polypeptide.

Please replace the paragraph on page 89, lines 8-14, with the following amended paragraph:

Another aspect of the invention is directed to the identification of agents capable of modulating the growth state of an IBD cell. In this regard, the invention provides assays for determining compounds that modulate the expression of the marker nucleic acids (~~SEQ ID Nos: 1-146~~ Table 1) and/or alter for example, inhibit the bioactivity of the encoded polypeptide.